В

61

IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG

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RESULT
Q62164
ID Qf
AC QC
DT 0
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Q1-NOV-1996 (Tremblr
Q1-NOV-1996 (Tremblr
Q1-OCT-2000 (Tremblr
ADENINE NUCLEOTIDE (
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01-OCT-2000
01-OCT-2000
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Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific
"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific Translocase mRNA Exhibits Specific Translocase of Expression During Development.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF231347; AAF63471.1; -.
                                                                    Q62164
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Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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Eukaryota; Metazoa; Chordata; Craniata;
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2000 (TrEMBLrel. 15, Last sequence update)
2000 (TrEMBLrel. 15, Last annotation update)
NUCLEOTIDE TRANSLOCASE.
            6 (TrEMBLrel. 01, 06 (TrEMBLrel. 01, 00 (TrEMBLrel. 15, CLEOTIDE CARRIER ()
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                                                                     PRELIMINARY;
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            Created)
Last sequence update)
Last annotation update)
(ADENINE NUCLEOTIDE TRANSLOCASE
                                                                                                                                                                                                                                                                                                                                                                Score 1421; DB 13;
Pred. No. 3.8e-122;
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Q9PRH1;
01-MAY-2000 (TrEMBLre
01-MAY-2000 (TrEMBLre
01-JUN-2000 (TrEMBLre
ADP/ATP TRANSLOCASE.
                                                                                                         Rana rugosa (Frog).
Eukaryota; Metazoa; Cl
Amphibia; Batrachia; I
NCBI_TaxID=8410;
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INTERPRO; IPR002067; -.
INTERPRO; IPR002113; -.
INTERPRO; IPR001213; -.
PRAM; PR00153; mito_cařr; 1.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL
EMBL; X74510; CAA52616.1; -.
EMBL; AF240002; AAF64470.1; -.
INTERPO; IRRO01993; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
"The Z, W,
                                          SEQUENCE FROM N.A.
Miura I., Ohtani H.,
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Submitted (SEP-1993)
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Local Similarity
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                       i H., Nakamura M., differentiation o
  the
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88.9%;
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frog
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Pred. No. 7.2e
19; Mismatches
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                                                                                                                                                                                                                                                                                                                   PRT;
                       ., Ichikawa Y., Saitoh of the heteromorphic
  rugosa,
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                                                                                                                                     Vertebrata;
a; Ranoidea;
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Ranidae; Rana
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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1254.5
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   US-09-393-441-33
1543
1 MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298
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Gapop 10.0 , Gapext 0.5
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Q9NHW5
Q44093
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046373 oryctolagus
Q919m9 xenopus lae
Q62164 mus musculu
Q9prh1 rana rugosa
Q919rh2 rana rugosa
Q9yic4 rana rugosa
Q9yic4 rana sylvat
Q9vz70 drosophila
Q9vz70 drosophila
Q9nw5 lucilia cup
Q44093 drosophila
Q25129 halocynthia
Q25129 halocynthia
Q25129 halocynthia
Q25120 caenorhabdi
P91410 caenorhabdi
P91410 caenorhabdi
Q45865 caenorhabdi
Q4597470 dictyosteli
Q1597470 dictyosteli
Q161813 caenorhabdi
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"The origin and differentiation of the heteromorphic sex chromosomes Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences ca sex-linked gene, ADP/ATP translocase.";
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F00153; mito_carr; 1.
PR00784; MTUNCOUPLING.
PR00926; MITOCARRIER.
PR00927; ADPTRNSLCASE.
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88.6%;
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Neobatrachia; Ranoidea;
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Pred. No. 4.8e-121;
9; Mismatches 15;
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annotation update)
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Ranidae; Rana
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Best Local Similarity 88.3
Matches 263; Conservative
                                                                                                                                                                                      INNER MEMBRANE (BY SIMILARITY)

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIE EMBL, ABO08457; BAA36507.1; -.

INTERPRO: IPR001993; -.

INTERPRO: IPR002030; -.

INTERPRO: IPR002067; -.

INTERPRO: IPR002113; -.

PRAM; PF00153; mito_carr; 1.

PRINTS; PR00784; MTUNCOUPLING.

PRINTS; PR00784; MTUNCOUPLING.

PRINTS; PR00926; MITOCARRIER.

PRINTS; PR00921; MITOCHARRIER.

PROSITE; PS00215; MITOCHARRIER: 3.

MITOCHONDRIAN REPEAT; Transmembrane; Transport.

MITOCHONDRIAN REPEAT; Transmembrane; Transport.

MITOCHONDRIAN REPEAT; Transmembrane; Transport.
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O1-MAY-1999 (TrEMBLrel. 1

O1-MAY-1999 (TrEMBLrel. 1

O1-MAY-2000 (TrEMBLrel. 1

ADP/ATP TRANSLOCASE.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana rugosa (Frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh "The origin and differentiation of the heteromorphic s W, X, and Y in the frog Rana rugosa, inferred from a sex-linked gene, ADP/ATP translocase.";
MOL. Biol. Evol. 15:1612-1619(1998).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99083429;
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                                                                                     Conservative
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Pred. No. 2.1e
21; Mismatches
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Pred. No. 9e-121;
O; Mismatches 15;
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annotation
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1.1e-120;
les 15;
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Ranidae; Rana
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Biochim.
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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72
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Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Ne
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Submitted (APR-1999)
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"Differential regulation of the mitochondrial ADP/ATP translocase gene in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
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INTERPRO; IPRO02067; -.
INTERPRO; IPRO02113; -.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                     MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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Neobatrachia; Ranoidea;
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2.8e-107;
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Ranidae; Rana
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RT "The genome sequence of Drosophila melanogaster.";
RD REMBL, AE003484, ARF47957.1; -.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S.; Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. A. A. H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. A. A. H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. A. A. H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. A. M. H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. M. M. H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. M. M. H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballow B. M. Bazna B. M. M. H.-J., Andrews-Ffannkoch C., Baldwin D.,
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                                                                                              FLYBASE; FBgn0003360; sesB.
INTERPRO; IPR001993; -.
INTERPRO; IPR002067; -.
INTERPRO; IPR002113; -.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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S; PR00926; MITOCARRIER
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SS MAL SEEKING; Chen Z., Fair J.A., Batterham P.; Chen Z., Fair J.A., Batterham P.; a cDNA clone encoding the ADP/ATP translocase of Lucilia Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF218587; AAF32322.1; SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
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Pterygota; Neoptera; Endopterygota;
Oestroidea; Calliphoridae; Lucilia.
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01-OCT-2000 (TremBLrel.
01-OCT-2000 (TremBLrel.
ADP/ATP TRANSLOCASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lucilia cuprina (Greenbottle
                                                                                                                129
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                                                                                                                GADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                 IYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMOSGRK
                                                                                                                                              TSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGII 185
                                                                                                                                                                             GFASYWRGNMANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFLGNLASGGAAGA
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79.5%;
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Pred. No. 6.7e-107;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fly) (Australian sheep blowfly).
3a; Tracheata; Hexapoda; Insecta;
rygota; Diptera; Brachycera; Musc
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NO. 3.7e-105;
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044094;
044094;
1 01-JUN-1998 (TrEMBLrel. 06, Create, Tr. 01-JUN-1998 (TrEMBLrel. 15, Last s.)
Tr. 01-OCT-2000 (TrEMBLrel. 15, Last a.)
ADP/ATP TRANSLOCASE (FRAGMENT).
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Query Match
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INTERPRO; IPR001993; -
INTERPRO; IPR002067; -
INTERPRO; IPR002133; -
INTERPRO; IPR00213; -
INTERPRO; IPR00213; -
PFAM; PF00153; mito_carr; 1.
PFAM; PF00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Repeat; Transmembrane; Tr
NON_TER 288 288
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044093;
044093;
01-UN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
anp/ATP TRANSLOCASE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila pseudoobscura (Fruit fly).
Eukaryota; Métazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                            INNER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATSLCFVYPLDFARTRLAADTGKGG-QREFTGLGNCLTKIFKSDGLVGLYRGFGVSVQGI 185
                                                                                                                                     ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLV
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80.7%;
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Pred. No. 8.6e-101;
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Tracheata; Hexapoda; Insecta;
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01-NOV-1996
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                             Q25129
Q25129;
                                                                                                                                                                                                               Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                  Miya
SEQUENCE FROM N.A.
Miya T., Makabe K., Satoh N.;
"Expression of a gene for major mitochondrial translocase, during embryogenesis in the ascic
                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAY-2000 (TrEMBLrel. 13, ADT/ATP TRANSLOCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Repeat; Transmembrane; Transport.
NON_TER 288 288
SEQUENCE 288 AA; 31775 MW; 06AlD1E477E81B26
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INTERPRO; IPRO02113; ...
PEAM; PFO0153; mito_carr; 1.
PRINTS; PRO0926; MITOCARRIER.
PRINTS; PRO0927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
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-i- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
Ephpdroidea; Drosophilldae; Drosophi
NCBI_TaxID-7241;
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EMBL: AF025799; AAB87884.1;
-FLYBASE; FEB00023237; DSub\sesB.
INTERPRO; IPR001993; -
                                                                                                                                                                       SEQUENCE
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80.4%;
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Drosophila.
                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
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                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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da; Tracheata; Hexapoda;
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                              protein,
                                                                                                                          databases
           Halocynthia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                              ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscomorpha;
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Best I
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01-AUG-1998
01-MAY-2000
Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Chentra A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         062526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00153; mito_carr; 1.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSICASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 304 AA; 33306 MW; 51FD0D7D6B654880
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Pterygota; Neoptera;
Ephydroidea; Drosoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev.
                                                                                                                                                                                                                                                                                                  STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D83069; BAA11765.1;
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
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Local Sir
hes 226;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
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                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arthropoda; Trac
Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
75
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Last sequence update)
Last annotation updat
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Pred. No. 9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      t fly).
a; Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Diptera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexapoda; Inso
a; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Insecta;
era; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
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RESULT
Q21103
ID Q7
AC Q7
DT 01
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RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyaum C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyaum C.,
RA Lin X., Mattei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lin X., Mattei B., KoIntosh T.C., McLeod M.P., Linang Y., Lin X.,
RA Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHon D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng S.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng S.H., Wallin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
R EMBL; AE003484; AAF47956.1; -
R EMBL; Y10618; CAA71629.1; -
R FLYBASE; FBgn0025111; Ant2.
R INTERPRO; IPR001993; -
R INTERPRO; IPR002067; -
R INTERPRO; IPR002113; -
R PFAM; PF00153; mito_CARTIER.
R PFINTS; PR00926; MITOCARRIER.
R PRINTS; PR00927; ADPENSICASE.
R PRINTS; PR00927; ADPENSICASE.
R PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 307 AA; 33744 MW; 3D6B3DFDB2061C0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 217; Conserv
  Q21103;
Q21103;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-OREGON-R;
                                                                                                                                    256
                                                                                                                                                                                                             196
                                                                                                                                                                                                                                                         187
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                                                                                                                                                                                                                                                                                                                                       127
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                                                                                                                                      YRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG
                                                                                                                                                                                                                                                                                            VLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSSFWRGNLANVIRYFPTQALNFAFKDVYKSVFLGGVDKHKQFWRHFAGNLASGGAAGAT
                                                                                                                                                                                                                 YRAAYFGFYDTCRDFLPNPKSTPFYVSWAIAQVVTTVAGIASYPFDTVRRRMMMQSGLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.78;
    01,
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    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1137.5;
Pred. No. 3.66
Pred. Mismatches
                                          313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                   255
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                                                                                                                                                                                                                                                                                              195
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  RESULT
P91410
ID P9
AC P9
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EMBL; 268218; CAA92472.1; -.
INTERPRO; IPRO1393; -.
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PRINTS; PRO0926; MITOCARRIER.
PRINTS; PRO0926; MITOCARRIER.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Walson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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01-MAY-2000 (TREMBLrel. 13, Last annotation
K01H12.2 PROTEIN.
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Caenorhabditis elegans.
Eukaryota Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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SEQUENCE 313
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PROSITE; PS00215; MITOCH_CARRIER; 3.

Mitochondrion; Repeat; Transmembrane; Transport.

SEQUENCE 313 AA; 34384 MW; D1E455DDB463C984 CRC64;
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                                                                                                                                                          ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADDTRNUSLCARE.
PRINTS; PR00927; ADDTRNUSLCARE.
PROSITE; PR00215; MITOCH_CARRIER; 3.
Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; U80931; AAB38001.1; -.
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STRAIN-BRISTOL N.2;
Geisel C., Stellyes L.;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.

NCBI_TaxID=6239;
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MEDLINE=94150718; PubMed=7906398;
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9; Mismatches 52;
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Search completed: April 29, 2001, 11:38:54 Job time: 154 sec

OM protein - protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:

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Title: Perfect score: Sequence:

US-09-393-441-33 1543 1 MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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EMBL; J03592; AAA36750.1; PIR; S03894; S03894. PIR; B28116; B28116. MIM; 300151; MIM; 403000; InterPro; IPR001993; InterPro; IPR002067; InterPro; IPR002113; Pfam; PF00153; mito_carr; 1. PRINTS; PR00926; MITOCARRIER. PRINTS; PR00927; ADPTRNSLCASE.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SEQUENCE OF 36-298 FROM N.A. SEQUENCE OF 36-298 FROM N.A. SEQUENCE OF 36-298 FROM N.A. TISSUE-Liver; MEDLINE-88124845; PubMed-2829183; Houldsworth J. Attardi G.; Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA "Two distinct genes for ADP/ATP t	nomo Septens (numen). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-89236396; PubMed-2541251; COzens A.L., Runswick M.J., Walker J.E.; "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase."; J. Mol. Biol. 206:261-280(1989).	UMAN DT3. HUMAN 12236; 1-0CT-1989 (1-NOV-1990 (1-NOV-1990 (1-NOV-1990 (DP, ATP CARRI ADENINE NUCL LC25A6 OR AN

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MEDLINE-89229093; PubMed-2540808;

Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;

"Two bovine genes for mitochondrial ADP/ATP translocase differences in various tissues.";
                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
ADP,ATP CARRIER PROTEIN, ISOFORM T2 (ADP/AT
NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
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  This SWISS-PROT entry is copyright. between the Swiss Institute of Bio.
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18534E9F0E49672F CRC64;
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Pred. No. 4.1e-130;
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(POTENTIAL).
                          MITOCHONDRIAL CARRIER FAMILY
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Best Loc
Matches
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InterPro; IPR002067; -.
InterPro; IPR002113; -.
Pfam; PF00153; mito_carr; 1.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADDTRNSLCASE.
SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=90375457; Pu
Ku D.-H., Kagan J.,
                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              HUMAN
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PubMed=2168878;
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Pred. No. 2.4e-127;
4; Mismatches 3;
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C.-D.,

Baserga

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cloning a J. Biol. [2]
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EMBL; 002683; AAA35579.1; --
EMBL; L78810; AAB39266.1; --
EMBL; AC004000; AAB96347.1; --
EMBL; J03591; AAA36749.1; --
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
                                                                                                                                                                                                                               InterPro; IPRO02067; -.
InterPro; IPRO02067; -.
InterPro; IPRO02113; -.
Pfam; PF00153; mito_carr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R., Mazzarella R.A., Schlessinger D., Chen E.Y.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth-regulated
J. Biol. Chem. 2
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                                          REPEAT
                                                     REPEAT
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SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
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(JAN-1998) to
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                                                                                                                                                                                         MITOCH_CARRIER;
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Calabretta B., Chen
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Best Local
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         EMBL; D12771;
InterPro; IPRO
InterPro; IPRO
                                                                                                                                                                                                                                                                                                                                                                               Q09073;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence updated)
01-OCT-2000 (Rel. 40, Last annotation updated)
ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFO
ADP,ATP MINGI-POTIDE TRANSLOCATOR 2) (ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADT2_RAT
Q09073;
                                                                                               the
                                                                                                                                                                                                                            "Isolation and characterization of cDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator."; Biochim. Biophys. Acta 1152:192-196(1993).
                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                         MEDLINE=94002161;
Shinohara Y., Kami
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                          SLC25A5 OR ANT2.
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European Bioinformatics Institute
                                                                                                                                        SKELETAL MUSCLE.
DOMAIN: COMPOSED OF
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                               SUBURIT: HOMODIMER.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                          TISSUE SPECIFICITY:
                                                                                                                                                                                                                    MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                       INNER MEMBRANE
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                                                                                             SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
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                                                 and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                   non-profit institutions as long
                    IPR001993;
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                                                                                                                                                                                                                                                                          Kamida M., Yamazaki N.,
                                                                                                                                                                                                                                                                                                         N.A.
                              BAA02238.1;
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92
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Pred. No. 5.4e-123;
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                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                    HOMOLOGOUS DOMAINS
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F973C3AED92C49D3 CRC64;
                                                                                                                                         MITOCHONDRIAL CARRIER FAMILY.
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                                                              http://www.isb-sib
                                                                                                                                                                          BRAIN,
                                                                                                                                                                                                                                                                                                                                          Muridae;
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                                                                         Usage
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for
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Best Local Similarity
                                                                                                                                                            ADT2_MOUSE STANDARD,

ADT2_MOUSE STANDARD,

P51881; Q61311;

01-OCT-1996 (Rel. 34, Created)

01-OCT-2996 (Rel. 34, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion; Inno
Multigene family.
TRANSMEM 12
TRANSMEM 73
TRANSMEM 176
TRANSMEM 176
TRANSMEM 214
TRANSMEM 273
REPEAT 112
REPEAT 12
REPEAT 209
SEQUENCE 298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF
PRINTS;
PRINTS;
                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                               TISSUE=Skeletal
Sheldon J.G.;
                                                                                         Ellison J.W.,
                                                                                               MEDLINE-97059403; PubMed-8903724;
                                                                                                          STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
SEQUENCE FROM N.A.
STRAIN=129/SV;
                                                                        "Rapid evolution homologs.";
                        Thesis
                                                SEQUENCE FROM
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=10090;
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s; pr00926; MITOCARRIER.
s; pr00927; ADPTRNSLCASE
                     (1995), University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                               7:25-30(1996).
                                                N.A.
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                                        muscle;
                                                                                                         TISSUE-Brain;
                                                                                 of human
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91
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111
111
298
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                                                                                        Francke U.,
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                        Of.
                                                                                 pseudoautosomal
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Pred. No. 6.3e-122
5; Mismatches 9
                       Cambridge,
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                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                        Shapiro L.J.;
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Best Local Similarity
Matches 271; Conser
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InterPro; IPR002067; -.
InterPro; IPR002113; -.
InterPro; IPR002113; mito_carr; I
Pfam; PF00153; mito_carr; I
PRINTS; PR00926; MITOCARRII
PRINTS; PR00927; ADPTRNSLC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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REPEAT
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Submitted
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U27316; AAC52838.1;
EMBL; U10404; AAA19009.1;
EMBL; X70847; CAA50196.1;
MGD; MGI:1353496; S1c25a5.
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                          QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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QSGRKGTDIMYTGTLDCWRKIARDEGSKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
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ted (FEB-1993) to the
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nilarity 91.6%;
Conservative 1
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TO THE MITOCHONDRIAL CARRIER
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Pred. No. 2.2e
L5; Mismatches
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EXCHANGE OF ADP AND ATP ACROSS
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Matches 267; Conserv
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SEQUENCE
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FCB-1994 (Rel. 28, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
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Q05962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding rat mitochondrial adenine nucleotide translocator.";
Biochim. Biophys. Acta 1152:192-196(1993).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAI
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Pfam; PF00153; mito_carr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY, AND WISTAR; TISSUE-Heart, MEDLINE-94002161; PubMed=8399300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                         Multigene
                                                                                                                                                                                                                                                                                                                    Mitochondrion;
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                PRINTS;
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EXTENT, IN BRAIN AND KIDNEY.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                              MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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| MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
          IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Swiss Institute of Bioinformatics
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                                                                                                      Conservative
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                                                                                                                  92.38;
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Pred. No. 1.6e
18; Mismatches
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                Transmembrane;
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thi; Muridae;
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                   EMBL; M13783; I
EMBL; M24102; I
EMBL; M24102; I
PIR; A03181; XI
PIR; A24822; A:
PIR; A43646; A:
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01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADT1_BOVIN P02722;
                                                                                                                                                                                                                                                        an unusually short 3'-noncoding sequence.";
Biochem. Biophys. Res. Commun. 138:850-857(1986)
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89229093; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial ADI differences in various tissues."; Biochemistry 28:866-873(1989).
                                                                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                        the
                                                                                                                                                               This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE
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                                                                                                                                                                                                                                                                                                                                                                 mitochondria
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=82188267;
                                                                                                                                                                                                                                                                                                        Rasmussen U.B.,
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                                                                                                                                       European
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                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                              MITOCHONDRIAL INNER MEMBRANE.
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D., Eulitz M., Klingenberg M.;
cid sequence of the ADP/ATP ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos.
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                                                                                                                                                                                    TO THE MITOCHONDRIAL CARRIER
                                                                                                                                                                                                THREE HOMOLOGOUS DOMAINS
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PIR; A43646; InterPro; IPI

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Best Local Similarity
Matches 265; Conser
                                                                                                                                                                                                                        MOUSE
                                                            STRAIN-C578L/6; TISSUE-Brain;
STRAIN-C578L/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
Ellison J.W., Li X., Francke U.,
                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
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Mamm. Genome 7:25-30(1996).

-i- FUNCTION: CATALYZES THE EXCHI-
-i- SUBUNIT: HOMODIMER.

-i- SUBUNIT: HOMODIMER.
                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
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Mulwigene family;
                                                      "Rapid evolution
                                                                                                                                                                                                    ADT1_MOUSE P48962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
                                             homologs.";
                                                                                                                                               SLC25A4 OR ANT1
                                                                                          SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                       AAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
                                                                                                                                                                                                                                                                                                                                                                            PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGG
                                                                                                                                                                                                                                                        AAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSV
                                                                                                                                                                                                                                                                                                                                                                   PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGG
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                                                      of human
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89.2%;
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 INTEGRAL
                                                      pseudoautosomal
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1 (POTENTIAL) :

2 (POTENTIAL) :

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4 (POTENTIAL) :

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6 (POTENTIAL) :

6 (POTENTIAL) :

1 :
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Pred. No. 6.6e-119;
9; Mismatches 13;
                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                             PRT;
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                                                              Shapiro L.
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MEMBRANE
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                                                               .J.;
                                                                                                                    Muridae;
PROTEIN.
                            AND
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                            ACROSS
MITOCHONDRIAL
                                                                                                                   Murinae;
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Best Local S
Matches 264
                                                                                                             L_HUMAN
ADT1_HUMAN
                                                                P12235;
01-OCT-1989
01-NOV-1990
01-OCT-2000
                                         01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE
TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
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REPEAT
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See Fertiles)
           Homo sapiens
Eukaryota; Me
                                  SLC25A4 OR ANT1
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U27315; AAC52837.1; -. MGD; MGI:1353495; Slc25a4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002067; -
InterPro; IPR002113; -
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                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                             INNER MEMBRANE
                                                                                                                                                                   QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
                                                                                                                                                                              QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                      VQGIIIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM
                                                                                                                                                                                                                                                         GAAGATSLCFYYPLDLARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                         IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                           Similarity 88.6
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00927; ADPTRNSLCASE.
PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e family.
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 Eutheria;
           Metazoa;
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                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner
                                                                                                             STANDARD;
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91
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 Primates;
            Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                          Score 1412; DB 1;
Pred. No. 1.9e-118;
9; Mismatches 15;
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Craniata; Ve
Catarrhini;
                                                                                                              PRT;
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(POTENTIAL).
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                                             TRANSLOCATOR
                                                                                                              298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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            Vertebrata;
 Hominidae;
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            Euteleostomi;
  Homo
                                                       11
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InterPro; IPR002067; ...
InterPro; IPR002067; ...
InterPro; IPR002113; ...
Pfam; PF00153; mito_carr; 1.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER
Mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CDNA sequence of a human skeletal muscle ADP/ATP translocator: of a leader peptide, divergence from a fibroblast translocator of a leader peptide, divergence from a fibroblast translocator and coevolution with mitochondrial DNA genes.";

Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
TRANSMEM
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                                                                   TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89340499; Pu
Li K., Warner C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cozens A.L., Runswick M.J., Wall "DNA sequences of two expressed ADP/ATP translocase.";
                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc.
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                                                                                                          Mitochondrion;
Multigene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88124845; PubMed=2829183;
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                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88041149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         level in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLINE-89340499; PubMed-2547778;
K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
kuyama R., Maekawa M., Shimizu N., Shimizu N., Wallace D.C.;
human muscle adenine nucleotide translocator gene has four of located on chromosome 4, and is differentially expressed.";
Biol. Chem. 264:13998-14004(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol.
                                                                                                                                                                                                                                         LL; J02966; AAA61223.1;
LI; J03593; AAA36751.1;
LL; J04982; AAA51736.1;
C; A28116; A28116.
C; A3891; A39891.
C; A3893; S03893.
C; A34778; A44778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           el in adult human liver.";
c. Natl. Acad. Sci. U.S.A. 85:377-381(1988)
FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: COMPOSED OF SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INNER MEMBRANE
                                                                                                                                                                                                                                103220;
                                                                                                          family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206:261-280(1989).
                                                                                                                       Inner membrane;
                                                                                                                                     ADPTRNSLCASE.
; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM
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K., Wade R.P.,
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TO THE MITOCHONDRIAL CARRIER FAMILY
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  21654321
                         (POTENTIAL).
(POTENTIAL).
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                                                                                                                       Repeat;
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                                                                                                                                     ω
                                                                                                                    Transmembrane;
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RESULT 10

ADT_DROME

ID ADT_DROME

AC Q26365; Q21

AC Q26365; Q21

AC Q26365; Q21

DT 15-JUL-199]

DT 15-JUL-199]

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DT 15-JUL-199]

ADP,ATP CATA

COMMANDATION

RET "A CDMA CLI

RET "A CDMA CLI

RET ADP/ATP tri

RA LOUVÍA.,

RA HUTTET P.,

RA SEQUENCE F.

RC STRAIN-ORE

RA SEDLINE-20

RA Adman M.D.

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CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q26365; Q26254; P91614; Q9VZ70;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-QCT-2000 (Rel. 40, Last annotation update)
ADP.ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
 Adams M.D., Celniker S.E., Holt Amanatides P.G., Scherer S.E., I
                             STRAIN-BERKELEY;
MEDLINE-20196006;
                                                                                          Zhang Y.Q.,
Submitted (
                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                 "Molecular analysis of a candidate isolation between sibling species (Experientia 50:749-762(1994).
                                                                                                                                                                                                                                                                                     melanogaster
ADP/ATP trans
                                                                                                                                                                                                                                                                                             LOUVI A., TSITIIOU S.U.,
"A CDNA clone encoding the ADP/ATP translocase
"A cDNA clone encoding the ADP/ATP translocase
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=92389367; PubMed=1387687;
                                                                                                                                                                                                                                                                                                                                                                                        Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
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                                                                                                                      STRAIN-OREGON-R;
                                                                                                                                                                                                             Hutter P., Karch F.;
                                                                                                                                                                                                                           MEDLINE=94350065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                                                                                                                                                                                     aster shows a high degree translocases."; Evol. 35:44-50(1992).
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53; Conservative
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; PubMed=10731132; iker S.E., Holt R.A Scherer S.E., Li F
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88.3%;
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KGA -> RR (IN REF. 3).

V -> L (IN REF. 3).

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9; Mismatches 16;
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             TRANSMEM CONFLICT
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                         PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          George R.A., Lewis S. Sutmon G.G., Wortman
                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                    InterPro; IPR002067;
                                                                                                                                                                                FlyBase; FBgn0003360;
InterPro; IPR001993; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brandon R.C., Rogers
                                                                                                                                                                                                                                                                                                                                                          DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                           PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., on R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., J.F., Agbayani A., An H.-J., Andrews-Pfannkock C., Baldwin D.,
                                                                                                                                                                                                      $43651; AAB23114.1; -. $71762; AAB31734.3; -. $710618; CAA71628.1; -. AE003484; AAF47957.1; -.
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Q27238;
Q1-NOV-1997
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                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
           EMBL; L11618; AAB04104.1; EMBL; L11617; AAB04105.1;
                                                                                                                                                                                                                                                        gambiae.
                                                                                                                                                                                                                                                                              MEDLINE=94348635; PubMed=8069414; Beard C.B., Crews-Oyen A.E., Kuma
                                                                                                                                                                                                                                                                                                                                         Culicidae; Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                          STRAIN-G3
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                                                                                                                                                                                                                                           Insect Mol. Biol. 3:35-40(1994)
                                                                                                                                                                                                                                                                 "A cDNA encoding
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                                                                                                                                                                                                     MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                                                                                                                   SIMILARITY:
                                                                                                                                                                             SUBCELLULAR LOCATION: INNER MEMBRANE.
                                                                                                                                                                                                                               FUNCTION: CATALYZES
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G -> A (IN REF. 2).
PC -> TGA (IN REF. 3 AND 4).
C -> S (IN REF. 1).
AA639439968F9750 CRC64;
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MITOCHONDRIAL CARRIER FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 233; Conserv
                                                                                                     Hilgarth C., Sauer N., Tanner W.;

"Glucose increases the expression of the AT glyceraldehyde-3-phosphate dehydrogenase ge J. Biol. Chem. 266:24044-24047(1991).

-I FUNCTION: CATALYZES THE EXCHANGE OF ADP MITOCHONDRIAL INNER MEMBRANE.

-I-* SUBUNIT: HOMODIMER (BY SIMILARITY).

-I-* SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                            CHLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion;
TRANSMEM 75
TRANSMEM 119
TRANSMEM 119
TRANSMEM 178
TRANSMEM 216
                                                                                                                                                                                                                                                                                                                        ADT_CHLKE
P31692;
01-JUL-1993
                                                                                                                                                                                                                                    Chlorella kessleri.
Eukaryota; Viridiplantae;
NCBI_TaxID=3074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00153; mito_carr; 1.
PRINTS; PR00926; MITOCARRIER;
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
MITOCH_CARRIER; 3.
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                                                                                                                                                                                                                                                                              TRANSLOCATOR)
                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=92084708; PubMed=1748677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002067;
InterPro; IPR002113;
                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                      DOMAIN: COMPOSED OF SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                          MMQSWPCKSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVKALL ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                 MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRIPKEQGIGAFWRGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLG
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77.7%;
                                                                     THREE HOMOLOGOUS DOMAINS.
TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                                                                                                                                                                                                                                   Chlorophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1204; DB 1
Pred. No. 6e-100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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(POTENTIAL)
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(POTENTIAL).
4CC9E17C9F8DA08B
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                                                                                                         MEMBRANE
                                                                                                                                                                                                                                                                                                                                                  339
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                                                                                                                                             ADP
                                                                                                                                                                  ATP/ADP translocator genes in Chlorella."
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                                                                                                                                             AND
                                                                                                          PROTEIN.
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                                                                                                                                                                                                                                                                                       (ADENINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                             ATP
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                                      a collaboration -
MBL outstation -
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Best Loc
Matches
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P18238;
01-NOV-1990
01-NOV-1990
01-OCT-1994
                                                                                                                                                                                                                                               YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP,ATP CARRIER PROTEIN 3 (ADP/ATP TRANSLOCAS
TRANSLOCATOR 3) (ANT 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00153; mito_Carr; 1.
PRINTS; PR00926; MITOCARRIER;
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
          Andre B.,
Vissers S.
                                                           SEQUENCE FROM N.A.
MEDLINE=90324269; PubMed=2165073;
Kolarov J., Kolarova N., Nelson N.;
"A third ADP/ATP translocator gene 1
J. Biol. Chem. 265:12711-12716(1990)
                                                                                                                                                    AAC3 OR YBR085W OR YBR0753.
Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                  Eukaryota; Fungi; l
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                STRAIN=S288C
                                        SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                         GAGSLLIVYPLDFARTRLAADVG-SGKSREFTGLVDCLSKVVKRGGPMALYQGFGVSVQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                               EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLFPKYSPK-TDFWRFFVVNLASGGLA
                                                                                                                                                                                                                                                                                                                                 IIVYRGAYFGLYDTAKGVLFKDERTANFFAKWAVAQAVTAGAGVLSYPFDTVRRRLMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M76669; AAA33027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement (See http://www.isb-sib.ch/announce/
                     Cziepluch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002067;
 (AUG-1994)
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108
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209
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                                                                                                                                evisiae (Baker's yeast).
Ascomycota; Saccharomycotina; Saccharomycetes;
; Saccharomycetaceae; Saccharomyces.
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126
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   EMBL/GenBank/DDBJ
                     c.,
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Pred. No. 8.6e-80;
6; Mismatches 64;
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                     Jauniaux J.C.,
                                                                     'n
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                      Urrestarazu
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Best Local S
Matches 161
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                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene family.
TRANSMEM 16
TRANSMEM 78
TRANSMEM 120
TRANSMEM 181
TRANSMEM 20
TRANSMEM 276
SEQUENCE 307 AA;
ADT_CHLRE
P27080;
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1994) to the EMBL/GenBank/DDBJ da-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C;
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SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: COMPOSED OF
                                                                                                                   MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                  PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S0000289; AAC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A36582; A36582.
                                                                                                                                              SVVGIVVYRGLYFGMFDSLKPLVLTGSLDGSFLASFLLGWVVTTGASTCSYPLDTVRRRM
                                                                                                                                                                       SVQGIIIYRAAYFGVYDTAKGM-LPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                          AAGATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSV
                                                                                                                                                                                                                                                    AKQEGLISFWRGNTANVIRYFPTQALNFAFKDKIKLMF--GFKKEEGYGKWFAGNLASGG
                                                                                                                                                                                                                                                                                                       QQETNFAINFLMGGVSAAIAKTAASPIERVKILIQNQDEMIKQGTLDKKYSGIVDCFKRT
                                                                                                                                                                                                                                                                                                                              EQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRI
                                                                                             MMTSGQA - -
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  (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                            STANDARD;
                                                                                           VKYNGAIDCLKKIVASEGVGSLFKGCGANILRSVAGAGVISMYDQLQMIL
23, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                                                                                                                                                       Score 778.5; DB 1;
Pred. No. 4.3e-62;
5; Mismatches 85;
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3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
COCC1329FEC1B4DC8 CRC64;
                             PRT;
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Matches 157; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Last sequence update) 01-OCT 1994 (Rel. 30, Last annotation updat ADP,ATP CHRRIER PROTEIN (ADP/ATP TRANSLOCAS TRANSLOCATOR) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002113; -.
Pfam; PF00153; mito_carr;
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InterPro; IPR001993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                                                                                                                                   RIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLAS 119
 RRMMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK
                            FNISCVGIVVYRGLYFGMYDSLKPVVLVGPLANNFLAAFLLGWGITIGAGLASYPIDTIR
                                                    FSVSVQGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR
                                                                                GGAAGAVSLSFVYSLDYARTRLANDAKSAKKGGGDRQFNGLVDVYRKTIASDGIAGLYRG
                                                                                                          GGAAGATSLCFVYPLDFARTRLAAD----VGKSGTEREFRGLGDCLVKITKSDGIRGLYQG
                                                                                                                                      RTVREEGFGSLWRGNTANVIRYFPTQALNFAFKDKFKRMF--GFNKDKEYWKWFAGNMAS
                                                                                                                                                                                            MAKEEKNFMVDFLAGGLSAAVSKTAAAPIERVKLLIQNQDEMIKQGRLASPYKGIGECFV
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Query Match Best Local

Similarity

49.8%;

Score 769; DB 1; Pred. No. 3.2e-61;

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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
TRANSLOCATOR) (ANT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyne M., Wood V., Rajandream M.A., Barrell B.G., Rieger M.; Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisia Gene 171:113-117(1996).
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Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.; "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schlzosaccharomyces pombe by functional complementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96257204; PubMed=8675018;
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Pfam; PF00153; mito_carr; 1.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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PR00927; ADPTRNSLCASE.
; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                                TSGEA---VKYSSSFECGRQILAKEGARSFFKGAGANILRGVAGAGVLSIYDQVQ 314
            QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK
                                                    VGIVVYRGLYFGMYDTLKPVVLVGPLEGNFLASFLLGWAVTTGSGVASYPLDTIRRRMMM
                                                                  QGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                        GAASLLFVYSLDYARTRLANDAKSAKKGGERQFNGLVDVYRKTYRSDGLRGLYRGFGPSV
                                                                                                                     GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
                                                                                                                                                            EEGVISLWRGNTANVLRYFPTQALNFAFKDKFKKMF-GYKKERDGYAKWFAGNLASGGAA 142
                                                                                                                                                                                    EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA 123
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	BB	ID	Description
1	1543	100.0	298	; سر	S03894	ADP, ATP carrier pr
2	1512	•	298	N	B43646	ATP carrier
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6	1418		298	N	S37210	ATP carrier
7	1409	٠-	298	۲	A44778	
80	1405	۳	298	N	S31814	carrier
9	1184	6.	301	_	S31935	
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11	1039	7	313	N	T25850	
12	1038	7.	300	N	T25371	
13	993.5		300	N	T15206	hypothetical prote
14	978	٠.	339	N	A41677	ADP, ATP carrier pr
15	943	۲	301	N	S51132	ADP, ATP
16	778.5		307	N	A36582	ADP, ATP carrier pr
17	772		308	Н	S30259	ATP carrier
18	769	9	322	N	T40526	adp/atp translocas
19	768	9.	386	N	T09709	ADP, ATP carrier pr
20	766	49.6	313	Ļ	XWNC	carrier
21	764	9.	326	N	T25728	tical pro
22	762.5	49.4	305	N	S68154	carr
23	760.5	49.3	318	_	A31978	ADP, ATP carrier pr
24	÷ 756.5		306	N	T20012	tical pro
25	750	48.6	387	N	S14876	carr
26	748		386	N	S21974	carrier
27	747	48.4	306	N	T42011	ADP, ATP carrier pr
28	747	48.4	386	N	S17917	ADP, ATP carrier pr
29	744	48.2	387	N	S16568	ADP, ATP carrier pr

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4.4 4.5	4 2 3	.40 41	39	38	37	36	<u>ა</u>	34	ω ω	32	31	30
344.5 321.5	369.5 368	372 370.5	381	383	520.5	681.5	734.5	737.5	739.5	742	742.5	743
22.3 20.8	23.9 23.8	24.1 24.0	24.7	24.8	33.7	44.2	47.6	47.8	47.9	48.1	48.1	48.2
332 479	381 475	358 415	352	325	327	298	379	309	386	382	385	379
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Ca-dependent solut peroxisomal Ca-dep	hypothetical prote peroxisomal Ca-dep	hypothetical prote hypothetical prote	mitochondrial solu	hypothetical prote	ADP/ATP translocas		٠	ADP, ATP carrier pr	٠	ADP, ATP carrier pr	carrier	ADP,ATP carrier pr

ALIGNMENTS

Qγ Ъ δÃ 망 F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3> A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein E;2-298/Product: ADP,ATP carrier protein #status predicted cMAT> R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level i A;Reference number: A94197; MUID:88124845
A;Accession: B28116... C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: S03894; B28116 A; Molecule type: mRNA A; Residues: 36-104,'R',106,'A',109-298 <HOU> A; Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723 A; Molecule type: DNA A; Residues: 1-298 <CO2> J. Mol. Biol. 206, 261-280, 1989 A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP A;Reference number: S03893; MUID:89236396 A;Accession: S03894 ADP,ATP carrier protein T3 - human N;Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP, A; Gene: GDB: ANT3; ANT3Y A;Experimental source: liver A;Status: not compared with conceptual translation R; Cozens, A.L.; Runswick, M.J.; Walker, J.E. Best Loc Matches Query Match
Best Local Similarity 61 61 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120 298; 100.0%; Score 1543; DB 1; llarity 100.0%; Pred. No. 6.4e-129; Conservative 0; Mismatches 0; Length 298; Gaps 0

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-298 cPOW>
A; Residues: 1-298 cPOW>
A; Residues: 1-298 cPOW>
A; Residues: 1-298 cpowable
A; Residues: 1-298 cpowable
A; Residues: 1-298 cpowable
A; Popularially: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C; Reywords: duplication; homodimer; mitochondrion; transmembrane protein
F; 5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP3>
F; 207-299/Domain: ADP, ATP carrier protein repeat homology <ACP3>
                                                                 R;Battini, R.; Ferrari, S.; Kaczmarck, L.; Calabretta, B.; J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP ca A;Reference number: A29132; MUID:87166056
A;Accession: A29132.
                                                                                                                                                           C;Date: 17-Mar-2000 #sequence_revision
C;Accession: A29132; C28116
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A;Title: Two bovine genes for mitochondrial A;Reference number: Ad3646; MUID:89229093
A;Accession: B43646
                   A; Molecule type: mRNA
A; Residues: 1-298 <BAT>
A; Cross references: GB:
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C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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     R; Houldsworth, J.;
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     Attardi,
   GB:J02683;
Attardi, G.
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97.7%;
                   NID:g179246;
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Pred. No. 3.5e-126;
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                   PIDN: AAA35579.1;
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Query Match
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Matches 267;
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A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier proteic;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI;207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI
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A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;Cross-references: GB.J03591; NII:g339720; PIDN:AAA36749.1;
A:Fxperimental source: clone pHAT3
                                                                                                                                                            A;Gene: antl
                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                     R;Shinohara, Y.; Kamida, M.; Yamazaki, N.;
Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of
A;Reference number: I60173; MUID:94002161
                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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A; Map position: Xq13-Xq26
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A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845
A;Accession: C28116
                                                                                                                                                                                                              A; Cross-references: EMBL: X61667;
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A; Residues: 1-298 < RES>
                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
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Pred. No. 4.7e-121;
.3; Mismatches 9;
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Similarity

92.3%; 89.6%;

Conservative

18;

Score 1424; D Pred. No. 2.1e 18; Mismatches

le-1 DB

18;

Indels

0

Gaps

0

Length

amino

acid;

mito

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A;Molecule type: mRNA
A;Residues: 208-298 KRAS>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID
R;Aquila, H; Misra, D; Eulitz, M; Klingenberg, M.
R;Aquila, H; Misra, D; Eulitz, M,; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A;Title: Complete amino acid sequence of the ADP/ATP carrier from the complete amino acid sequence of the ADP/ATP carrier from the complete protein
A;Reference number: A03181; MUID:82188267
A;Residues: 2-51, 'x', 53-70, 'x', 72-109, 'x', 111-298 <AQU>
A;Rote: residues: 2-51, 'x', 53-70, 'x', 72-109, 'x', 111-298 <AQU>
A;Rote: residue 52 may be methyllysine
B;Babel, W; Wachter, E; Aquila, H; Klingenberg, M.
Biophys. Acta 670, 176-180, 1981
A;Title: Amino acid sequence determination of the ADP, ATP carrier
A;Reference number: A61343; MUID:82046808
A;Accession: A61343
A;Accession: A61343; MUID:82046808
                                                        A; Molecule type: protein
A; Residues: 205-298 < CABD.
R; Oettmeler, W.; Masson, K.; Kalinna, S.
Eur: J. Biochem. 227, 730-733, 1995
A; Title: [(3)H]7-azido-4-isopropylacridone la
A; Reference number: S69369; MUID:95172058
A; Accession: S69369
A; Molecule type: protein
A; Residues: 49-63; 154-168 <OET>
A; Comment: This protein is synthesized in the C; Commlex: homodimer
C; Comment: This protein is synthesized in the C; Complex: homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093
A;Accession: A43646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M24102; NID:g529414; PIDN:AAA307 R;Rasmussen, U.B.; Wohlrab, H. Biochem. Biophys. Res. Commun. 138, 850-857, 1986 A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: A;Reference number: A24822; MUID:86295775
  A; Note: located C; Superfamily: 1
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A;Description: catalyzes the exchange between cytosolic A;Note: located in the inner mitochondrial membrane C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier
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A; Accession: A24822
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A; Residues: 1-298 < POW>
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C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein C;Keywords: duplication; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S37210
R; Laplace, C.; Costet, P.
submitted to the EMBL Data
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
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A; Residues: 1-298 < LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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89.3%; Pred. No. 3.2e-118;
Live 19; Mismatches 13;
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A;Map position: 4q35-4q35
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Tille: Two distinct genes for ADP/ATP translocase
A;Reference number: A94197; MUID:88124845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNĀ A;Residues: 1-15,'A',17-146,'RR',149,151-226,'L',228-298 <NEC>A;Residues: 1-15,'A',17-146,'RR',149,151-226,'L',228-298 <NEC>A;Croos-references: GB.J02966; NID:9339919; PIDN:AAA61223.1; PA;Experimental source: clone pHMANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A; Title: cDNA sequence of a human skeletal muscle ADP/ATP t. A; Reference number: A39891; MUID:88041149
A; Accession: A39891
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A;Title: DNA sequences of two expressed nuclear genes for hum A;Reference number: S03893; MUID:89236396
A;Accession: S03893
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A; Residues: 1-37 <HOU>
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                                                                                                                                                                                                                                           Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat Keywords: duplication; homodimer; mitochondrion; transmembrane protein; 2-298/Product: ADP,ATP carrier protein #status predicted <MAT>;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP2>
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Best Local Similarity
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                                                                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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                                              MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                       Conservative
                                                                                                                                                       91.3%;
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                                                                                                                                       19;
                                                                                                                                     Score 1409; DB 1;
Pred. No. 4.5e-117;
9; Mismatches 16;
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A.Cross references: EMBL:X70847
A.Cross references: EMBL:X70847
C.Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat: C.Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                   R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier
                                                                                     ADP.ATP carrier protein - African malaria mosquito (C;Species: Anopheles gambiae (African malaria mosquito) (C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: S31935; S31936
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A; Residues: 1-298 < COS>
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S31814
ADP, ATP carrier protein T2
  A; Reference number:
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S31935
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Pred. No. 1e-116;
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A; Map position:
A; Introns: 4/1;
C; Superfamily: A
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
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                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-313 <WIL>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K01H12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated
                                                                                                                                                                                                                     Query Match
Best Local
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                  LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                       LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                              FAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTKKADPYGFAKDFLAGGISAAVSKTAVAPIERVKLLLQVQAASKQIAVDKQYKGIVDCF 60
                                                    AALWRGNLANVIRYEPTQALNEAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                           FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY 84
 T23207
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77.08;
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70.9%;
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Score 1041; DB 2;
Pred. No. 1.6e-84;
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Pred. No. 3
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RESULT
T25850
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted to the EMBL Data Library, December 1990 A:Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T01B11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
                                                                                                                                                                                      hypothetical protein T27E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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                                                                                                      submitted to the EMBL Data A; Reference number: Z20024
                                                                                                                                             R; Lloyd,
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A; Residues: 1-313 <GEI>
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  A; Cross-references:
                                         A; Molecule type: DNA
                                                          A; Status: preliminary; translated from
                                                                                  A; Reference number: A; Accession: T25371
                       ;Residues: 1-300 <WIL>
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                                                                                                                                                                                                                                                                                                                                        -DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
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EMBL: Z82059; PIDN: CAB04874.1; GSPDB: GN00021; CESP: T27E9.1
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hypothetical protein W02D3.6 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tc C.Accession: T15206 R.Le, T.; Weinstock, L.; Rifkin, L.
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C:Superfamily: ADP,ATP carrier protein;
F;9-103/Domain: ADP,ATP carrier protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans co A;Reference number: Z18308
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A;Introns: 20/1; 41/3; 115/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
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179 VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRR
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                                                                                                                  VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                               SGGAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                  ARVPKEQGYAAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA
                                                                                                                                                                      TKEGFDYRKFLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVL
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                               SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF
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64.8%;
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; Pred. No. 2.8e-84;
37; Mismatches 49;
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Pred. No. 2.4e-80;
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S51132
                            A; Reference number: S68993;
A; Accession: S68993
                                               A; Title: Molecular characterisation of the A; Reference number: S68993; MUID: 95188918
                                                                                 R; Hatin, I.; Jaureguiberry, G. Eur. J. Biochem. 228, 86-91, 1
                                                                                                                               C;Species: Plasmodium falciparum
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995
                                                                                                                                                                  N; Alternate names: ADP/ATP transporter
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              A; Status: preliminary
                                                                                                               C; Accession: $68993; $51132
                                                                                                                                                                                  ADP, ATP carrier protein - malaria parasite
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A;Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat ht C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;38-134/Domain: ADP,ATP carrier protein repeat homology <ACPl>F;144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Ju
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A41677
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A; Residues: 1-339 <HIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Glucose increases the expression A; Reference number: A41677; MUID:92084708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 266, 24044-24047,
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                     GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                      IIIYRAAYFGYYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
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---GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKFI
                                                                                GAGSLLIVYPLDFARTRLAADVG-SGKSREFTGLVDCLSKVVKRGGPMALYQGFGVSVQG
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                                                                                                                                                                                                                                                                                             EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA 123
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Pred. No. 6.4e-79;
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ADP/ATP-transporter

CDNA

from the human

ma

(Plasmodium

#text_change 09-Jun-2000

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A:Residues: 1-301 <HAT>
A:Residues: 1-301 <HAT>
A:Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C:Keywords: duplication; transmembrane protein
F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
Search completed: April 29, 2001, 11:38:21 Job time: 156 sec
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                                                                              68 QGVLSLWRGNVANVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILSGATAG 126
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(c) 1993 - 2000 Compugen Ltd
908.514 Million cell updates/sec
                          (without alignments)
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Title: US-09-393-441-33 1543

Perfect score: Sequence: MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters:

390729

Minimum DB DB

Maximum seq seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

A_Geneseq_0401:*

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2: /SIDS6/gcgdata,

3: /SIDS6/gcgdata,

4: /SIDS6/gcgdata,

5: /SIDS6/gcgdata,

6: /SIDS6/gcgdata,

7: /SIDS6/gcgdata,

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pring and is derived by analysis of the total score distribution. being printed,

SUMMARIES

Result	Query	
1 ₩ 1543	298 21	Human adenine nucl
2 1454	94.2 298 21 Y71032	
3 1412	298 19	
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5 742.5	346 21	_
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9 742.5	363 21	Arabidopsis thalia
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(MITO-) MITOKOR. 03-NOV-1998; 08-SEP-1999;

98US-0185904 99US-0393441

369.5 23.	69.5 2	70.5 2	381 2	82 3	518 3	63.5 3	72.5 3	84.5 3	85.5 3	.5	88.5 3	54 4	654 4	58.5 4	.5	672 43	672 43	.5 4	79.5 44	79.5 44	88.5 44	89.5 44	39.5 47	39.5 4	39.5 4	42.5 4	42.5 4	42.5 4	42.5 4	42.5 4	42.5 4	42.5 4	42.5 4
9 384 21	381 2	415 2	352 2	200 2	132 2	228 2	312 2	249 2	249 2	263 2	263 2	291 2	291 2	291 2	291 2	306 2	306 2	368 2	350 2	333 2	330 2	330 2	381 2	363 2	346 2	1027 2	1009 2	992 2	381 2	381 2	381 2	381 2	363 2
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ALIGNMENTS

Y71033 Human adenine nucleotide translocator ANT3. 29-AUG-2000 Y71033; Y71033 standard; (first entry) Protein; 298 ₹

Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; 03-NOV-1999; WO200026370-A2 Homo sapiens. myoclonic epilepsy red 11-MAY-2000 99WO-US25883 ragged fibre syndrome

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                                                      adenosine di-phosphate;
mitochondrial permeabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, useful e.g. in screening against mitochondrial disease
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N-PSDB; D00521.
                        antiParkinsonian;
                                                                                                                   Human;
                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein;
                                                                                                          adenine nucleotide translocator; ANT2;
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                                                                                                                                                                                                                                 (first entry)
                                    e nucleotide translocator; ANT2; mitochondria; ADP; Aphosphate; adenosine tri-phosphate; apoptosis; MPT; c permeability transition; neuroprotective; nootropic; ian; cytostatic artistation;
                                                                                                                                                                       nucleotide translocator ANT2
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                        cytostatic; antidiabetic; anticonvulsant;
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                           neuroleptic
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                                                                                  cancer;
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Db Qy

121

121

GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

180

240

Qy Qy

QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK

VQGIIIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM

vqgiiiyraayfgiydtakgmlpdpknthiviswmiaqtvtavagltsypfdtvrrrmmm

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                                                                     Вb
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                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of ademosine di/tri-phosphates across the mitochondrial inner membrane and also set as an important molecular component of the mitochondrial permeability transports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                     transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant construct encoding adenimpolypeptide, useful e.g. in screening against mitochondrial disease
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08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 45; Page 172-173; 175pp; English.
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                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease; Parkinson's disease; Huntington's disease;
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   61
                                    61
                                                                                       1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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                  IPKEQGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                     mtdaalsfakdflaggvaaaisktavapiervklllqvqhaskqitadkqykgiidcvvr
ip ke qevls fwrgnlanviry fpt qaln fafkdkyk qifl ggvdkrtq fwry fagnlasg
                                                                                                                                           274;
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                                                                                                                                           Conservative
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                                                                                                                                                                                                                                 AA;
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99US-0393441
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92.6%;
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                                                                                                                                     Score 1454; Db ....
Pred. No. 6.5e-148;
Pred. No. -hes 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenine nucleotide translocator reening for potential therapeutic agents
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                                                                                                                                           Gaps
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                                                                                                                  Query Match
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Matches 264
                                                                                                                                                                                                                           The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OxPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                     independent of ANT1.
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                                                       \verb|mgdqalsflkdflaggiaaavsktavapiervklllqvqhaskqisaekqykgiidcvvr|
                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                    264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acidosis;
                                                                                                                                                                                         298 AA
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                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degenerative muscle disease.
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Pred. No. 2.1e-143;
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              The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neurolep antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystralzheimer's dystralzheimer's dystralzheimer's dys
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic against mitochondrial disease \,\,
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Ghosh SS;
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                                                                                                                                                                                                                                                                                                                                                                                              Page 172;
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hereditary optic neuropathy,

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Best Local Similarity 87.2%;
Matches 260; Conservative
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                                                                                                                                                                                                                                                                                                    Protein identification; signal hybridisation assay; genetic matermination sequence.
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  990S-0121825

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990S-0126765

990S-0128234

990S-0128234

990S-0128945

990S-0130049

990S-0130440

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Pred. No. 1.5e-140;
1; Mismatches 16; 1
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promoter;
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                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                               06-SEP-2000.
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160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                              thaliana protein fragment SEQ ID NO: 45788
                                                                                                          2000EP-0301439
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99US-0121825.
99US-0123180.
99US-0123548.
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990S-0160814.
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                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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RESULT 8

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                                                                                                                                                                                                                                                     160;
                                                       standard;
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Similarity 52.8%;
60; Conservative '
                                                                                                                       298
                                                                                                      353
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                   990S-0157117

990S-0157865

990S-0158029

990S-0158329

990S-0159293

990S-0159295

990S-0159295

990S-0159329

990S-0159331

990S-0159331

990S-0160741

990S-0160741

990S-0160768

990S-0160768

990S-0160815

990S-0160815

990S-0160815

990S-0161081

990S-01611404

990S-01611405

990S-01611920

990S-01611920
                                                       Protein;
                                                       381
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                                                                                                                                                                                                                                                                                                                               Score 742.5;
Pred. No. 2.1e
15; Mismatches
                                                       ΑA
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nes 77;
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02-AUG-1999 03-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999

990S-0143442
990S-0144005
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990S-0144331
990S-0144333
990S-0144333
990S-0144333
990S-0144333
990S-0145086
990S-0146884
990S-0147303

02-AUG-1999; 02-AUG-1999; 02-AUG-1999;

26-JUL-1999; 27-JUL-1999; 27-JUL-1999;

27-JUL-1999, 28-JUL-1999,

22-JUL-1999; 22-JUL-1999; 23-JUL-1999;

23-JUL-1999; 23-JUL-1999;

21-JUL-1999; 21-JUL-1999; 21-JUL-1999;

20-JUL-1999; 20-JUL-1999;

19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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13-AU-16-AUG-1995; 8 17-AUG-1999; 18-AUG-1999; "G-1996

11-AUG-1 12-AUG-1 13-AUG-1

-1999 999

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990S-0139456. 990S-0139456. 990S-0139458. 990S-0139458. 990S-0139460. 990S-0139461. 990S-0139462. 990S-0139463. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763.	990S-0135124 990S-0135124 990S-0135629 990S-0136621 990S-0136392 990S-0136722 990S-0137528 990S-0137528 990S-0137524 990S-0137524 990S-013914 990S-0139147 990S-0139147 990S-0139149 990S-0139453	990S-0130449. 990S-0130810. 990S-0131449. 990S-01324048. 990S-0132484. 990S-0132486. 990S-0132486. 990S-0132487. 990S-0134218. 990S-0134218. 990S-0134218. 990S-0134218. 990S-0134218.	identification; signal tation assay; genetic map ion sequence. sis thaliana. 5-A2. 5000. 2000EP-0301439. 999; 99US-0121825. 999; 99US-0125788. 999; 99US-0125788. 999; 99US-0126264. 999; 99US-012627462. 999; 99US-0128234. 999; 99US-0128234. 999; 99US-0128234. 999; 99US-0128714. 999; 99US-0128714. 999; 99US-01287077.
			signal transduction pathwa etic mapping; gene express 180. 180. 548. 7548. 7548. 714. 862. 439.
			ion control;
	•		<pre>pathway; promoter;</pre>
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-0149175 -0149426 -0149723 -0149723 -0149929 -0149930 -0150864 -0151065 -0151066 -0151066			99US -0140353 99US -0140695 99US -0140691 99US -0141287 99US -01412154 99US -0142154 99US -0142154 99US -0142803 99US -0142803 99US -014290 99US -014290 99US -014297 99US -014297 99US -014292 99US -014293 99US -0143624 99US -0144085 99US -0144331 99US -0144333 99US -0144333 99US -0144333

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Query Match 48.1
Best Local Similarity 52.8
Matches 160; Conservative
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26-OCT-1999;
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01-SEP-1999;
07-SEP-1999;
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29-SEP-1999,
      296 KVI
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G37259
        Дb
  05-MAR 1999
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23-MAR 1999
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28-MAY 1999
29-MAY 1999
21-MAY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S-0121825
990S-0123548
990S-0125788
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990S-012578
990S-0126785
990S-0128714
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Matches 160; Conservative
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3-AUG-1999;
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5-AUG-1999;
5-AUG-1999;
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                                                                                                                                     ; Score 742.5; DB 21; pred. No. 2.2e-71; 45; Mismatches 77;
                                                                                                                                         Indels
                                                                                                                                                                       Length
                                                                                                                                                                         381;
                                                                                                                                         21;
                                                                                                                                       Gaps
                                       123
     195
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                                                                                                                                         7;
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18-JUN-1999
19-JUN-1999
10-JUN-1999
11-JUN-1999
11-JUN

9908-0139455
9908-0139458
9908-0139459
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RESULT
G37262
  09-MAR-1999
23-MAR-1999
25-MAR-1999
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